

SEQUENCE LISTING

<110> Andrew, David P.
Zabel, Brian A.
Ponath, Paul D.

<120> ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION

<130> LKS98-16

<140> 09/266,464
<141> 1999-03-11

<160> 7

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2577

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58

<400> 1

aatattttcc ttgaccta at gccatcttgt gtccccttgc agagccstat tccttaac atg 60
Met
1

aac ttc aac ttc act gac ttc tac tgt gag aaa aac aat gtc agg cag 156
 Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln
 20 25 30

ttt gcg agc cat ttc ctc cca ccc ttg tac tgg ctc gtg ttc atc gtg 204
 Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val
 35 40 45

ggt gcc ttg ggc aac agt ctt gtt atc ctt gtc tac tgg tac tac tgc aca	252		
Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr			
50	55	60	65

aga gtg aag acc atg acc gac atg ttc ctt ttg aat ttg gca att gct 300
Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala
70 75 80

gac ctc ctc ttt ctt gtc act ctt ccc ttc tgg gcc att gct gct gct	348
Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala	
85 90 95	
gac cag tgg aag ttc cag acc ttc atg tgc aag gtg gtc aac agc atg	396
Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met	
100 105 110	
tac aag atg aac ttc tac agc tgt gtg ttg ctg atc atg tgc atc agc	444
Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser	
115 120 125	
gtg gac agg tac att gcc att gcc cag gcc atg aga gca cat act tgg	492
Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp	
130 135 140 145	
agg gag aaa agg ctt ttg tac agc aaa atg gtt tgc ttt acc atc tgg	540
Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp	
150 155 160	
gta ttg gca gct gct ctc tgc atc cca gaa atc tta tac agc caa atc	588
Val Leu Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile	
165 170 175	
aag gag gaa tcc ggc att gct atc tgc acc atg gtt tac cct agc gat	636
Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp	
180 185 190	
gag agc acc aaa ctg aag tca gct gtc ttg acc ctg aag gtc att ctg	684
Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu	
195 200 205	
ggg ttc ttc ctt ccc ttc gtg gtc atg gct tgc tgc tat acc atc atc	732
Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile	
210 215 220 225	
att cac acc ctg ata caa gcc aag aag tct tcc aag cac aaa gcc cta	780
Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu	
230 235 240	
aaa gtg acc atc act gtc ctg acc gtc ttt gtc ttg tct cag ttt ccc	828
Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro	
245 250 255	
tac aac tgc att ttg ttg gtg cag acc att gac gcc tat gcc atg ttc	876
Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe	
260 265 270	
atc tcc aac tgt gcc gtt tcc acc aac att gac atc tgc ttc cag gtc	924
Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val	
275 280 285	
acc cag acc atc gcc ttc ttc cac agt tgc ctg aac cct gtt ctc tat	972
Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr	
290 295 300 305	

gtt ttt gtg ggt gag aga ttc cgc cg ^g gat ctc gtg aaa acc ctg aag	1020
Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys	
310	315
320	
aac ttg ggt tgc atc agc cag gcc cag tgg gtt tca ttt aca agg aga	1068
Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg	
325	330
335	
gag gga agc ttg aag ctg tcg tct atg ttg ctg gag aca acc tca gga	1116
Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly	
340	345
350	
gca ctc tcc ctc tga ggggtttct ctgaggtgca tgggtttttt ggaagaaatg	1171
Ala Leu Ser Leu *	
355	
agaaaatacat gaaacagttt ccccactgat gggaccagag agagtggaaag agaaaagaaaa	1231
actcagaaag ggatgaatct gaactataatg attacttgc gtcagaattt gccaaagcaa	1291
atatttcaaa atcaactgac tagtgcagga ggctgttgat tggcttttga ctgtgatgcc	1351
cgcaattctc aaaggaggac taaggaccgg cactgtggag caccctggct ttgccactcg	1411
ccggagcatc aatgccgtg cctctggagg agcccttgg ttttctccat gcactgtgaa	1471
cttctgtggc ttcatgttctc atgctgcctc ttccaaaagg ggacacagaa gcactggctg	1531
ctgctacaga ccgcaaaags agaaagtttgc gtgaaaatgt ccattttgg gaaattttct	1591
accctgctct tgagcctgat aacccatgcc aggtttata gattcctgat ctggaaacctt	1651
tccaggcaat ctcagaccta atttccttctt gttctccttgc ttctgttctg ggccagtgaa	1711
ggtccttggc ctgattttga aacgatctgc aggttttgc agtggaaaccc tggacaactg	1771
accacaccca caaggcatcc aaagtctgtt ggcttccat ccattttgtt gtcctgtgg	1831
aggtttaac ctagacaagg attccgccta ttcccttggta tgggtgacagt gtctctccat	1891
ggcctgagca gggagattt aacagctggg ttgcgcaggag ccagccttgg ccctgttgc	1951
ggcttgcgtt gttgagtttgc acttgcattt ggtccaccgt ctgtctgc cctagaaaat	2011
gggctgggttc ttttggccctt cttctttctg aggcccactt tattctgagg aatacagtga	2071
gcagatatgg gcagcagccaa ggttagggcaa aggggtgaag cgcaggcctt gctggaaaggc	2131
tatttacttc catgcttctc cttttcttac tctatagtgg caacatttttta aaagctttta	2191
acttagagat taggctgaaa aaaataagta atgaaattca cctttgcattc ttttgcgttct	2251
ttcttatcat gatttggcaa aatgcattcac ctttggaaat atttcacata ttggaaaatg	2311
gcttttaat gtgtatatga agcattaatt acttgcattt ttcttttaccc tgcgttcaata	2371
ttttaagtgt gtgcaattaa agatcaaata gatacattaa gagtgtgaag gctggcttgc	2431
aggtagtgag ctatctcaat cggatttttc acactcattt acagattgaa ctccttgc	2491
tacttccctg cttctctcta ctgcaatttgc ctgttttttta aaaaaaaatgt tgaagagttaa	2551
gcaataggaa taaggaaata agatct	2577

<210> 2
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
 1 5 10 15
 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg
 20 25 30
 Gln Phe Ala Ser His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile
 35 40 45
 Val Gly Ala Leu Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys
 50 55 60

Thr Arg Val Lys Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile
 65 70 75 80
 Ala Asp Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala
 85 90 95
 Ala Asp Gln Trp Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser
 100 105 110
 Met Tyr Lys Met Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile
 115 120 125
 Ser Val Asp Arg Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr
 130 135 140
 Trp Arg Glu Lys Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile
 145 150 155 160
 Trp Val Leu Ala Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln
 165 170 175
 Ile Lys Glu Glu Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser
 180 185 190
 Asp Glu Ser Thr Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile
 195 200 205
 Leu Gly Phe Phe Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile
 210 215 220
 Ile Ile His Thr Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala
 225 230 235 240
 Leu Lys Val Thr Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe
 245 250 255
 Pro Tyr Asn Cys Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met
 260 265 270
 Phe Ile Ser Asn Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln
 275 280 285
 Val Thr Gln Thr Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu
 290 295 300
 Tyr Val Phe Val Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu
 305 310 315 320
 Lys Asn Leu Gly Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg
 325 330 335
 Arg Glu Gly Ser Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser
 340 345 350
 Gly Ala Leu Ser Leu
 355

<210> 3
 <211> 26
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> NH2-Terminal Peptide of Human GPR-9-6

<400> 3
 Met Ala Asp Asp Tyr Gly Ser Glu Ser Thr Ser Ser Met Glu Asp Tyr
 1 5 10 15
 Val Asn Phe Asn Phe Thr Asp Phe Tyr Cys
 20 25

<210> 4
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 4
tcgaaggat ccctaacatg gctgatgact atggc

35

<210> 5
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 5
aagaagtcta gaaccctca gagggagagt gctcc

35

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 6
tcgaagaagc ttatgaacct gtggctcctg

30

<210> 7
<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 7

aagaagtcta gatcacagtc ctgaattagc

30